



#3

1

## SEQUENCE LISTING

<110> BAUBET, VALERIE  
LE MOUELLIC, HERVE  
BRULET, PHILIPPE

<120> CHIMERIC GFP-AEQUORIN AS BIOLUMINESCENT Ca++ REPORTERS  
AT THE SINGLE CELL LEVEL

<130> 03495-0207-00000

<140> 09/863,901

<141> 2001-05-24

<150> 60/208,314

<151> 2000-06-01

<150> 60/210,526

<151> 2000-06-06

<150> 60/255,111

<151> 2000-12-14

<160> 48

<170> PatentIn Ver. 2.1

<210> 1

<211> 432

<212> PRT

<213> Aequorea victoria

<400> 1

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
	130					135					140						
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
145					150					155					160		
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
				165					170					175			
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
			180					185					190				
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser		
	195						200					205					
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val		
	210					215					220						
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Gly		
225					230					235					240		
Leu	Arg	Ser	Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	Pro	Arg	Trp	Ile		
				245					250					255			
Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	Asn	His	Asn	Gly		
			260					265					270				
Lys	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	Asp	Ile	Val	Ile		
		275					280					285					
Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	His	Lys	Asp	Ala		
	290					295					300						
Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	Gly	Val	Glu	Thr		
305					310					315					320		
Asp	Trp	Pro	Ala	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	Ala	Thr	Asp	Glu		
				325					330					335			
Leu	Glu	Lys	Tyr	Ala	Lys	Asn	Glu	Pro	Thr	Leu	Ile	Arg	Ile	Trp	Gly		
			340					345						350			
Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	Gly	Ala	Ile	Thr		
		355					360					365					
Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	Ile	Ile	Gln	Ser		
	370					375					380						
Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile	Asp	Glu	Ser		
385					390					395					400		
Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu	Gly	Phe	Trp		
				405					410					415			
Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Gly	Ala	Val	Pro		
			420					425					430				

&lt;210&gt; 2

&lt;211&gt; 441

&lt;212&gt; PRT

&lt;213&gt; Aequorea victoria

&lt;400&gt; 2

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly  
 225 230 235 240

Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu Arg Ser Val Lys Leu Thr  
 245 250 255

Ser Asp Phe Asp Asn Pro Arg Trp Ile Gly Arg His Lys His Met Phe  
 260 265 270

Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met  
 275 280 285  
 Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro  
 290 295 300  
 Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly  
 305 310 315 320  
 Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu  
 325 330 335  
 Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn  
 340 345 350  
 Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val  
 355 360 365  
 Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr  
 370 375 380  
 Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr  
 385 390 395 400  
 Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu  
 405 410 415  
 Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys  
 420 425 430  
 Glu Lys Leu Tyr Gly Gly Ala Val Pro  
 435 440

<210> 3  
 <211> 450  
 <212> PRT  
 <213> Aequorea victoria

<400> 3  
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60  
 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	100	105	110	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	115	120	125	
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	130	135	140	
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	145	150	155	160
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	165	170	175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	180	185	190	
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	195	200	205	
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	210	215	220	
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Gly	225	230	235	240
Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	245	250	255	
Ser	Gly	Leu	Arg	Ser	Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	Pro	Arg	260	265	270	
Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	Asn	His	275	280	285	
Asn	Gly	Lys	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	Asp	Ile	290	295	300	
Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	His	Lys	305	310	315	320
Asp	Ala	Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	Gly	Val	325	330	335	
Glu	Thr	Asp	Trp	Pro	Ala	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	Ala	Thr	340	345	350	
Asp	Glu	Leu	Glu	Lys	Tyr	Ala	Lys	Asn	Glu	Pro	Thr	Leu	Ile	Arg	Ile	355	360	365	
Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	Gly	Ala	370	375	380	
Ile	Thr	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	Ile	Ile	385	390	395	400

Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp  
 405 410 415

Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu Gly  
 420 425 430

Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala  
 435 440 445

Val Pro  
 450

<210> 4

<211> 468

<212> PRT

<213> *Aequorea victoria*

<400> 4

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220  
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly  
 225 230 235 240  
 Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln  
 245 250 255  
 Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly  
 260 265 270  
 Gly Gln Ser Gly Leu Arg Ser Val Lys Leu Thr Ser Asp Phe Asp Asn  
 275 280 285  
 Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val  
 290 295 300  
 Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser  
 305 310 315 320  
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg  
 325 330 335  
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr  
 340 345 350  
 Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu  
 355 360 365  
 Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile  
 370 375 380  
 Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn  
 385 390 395 400  
 Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly  
 405 410 415  
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp  
 420 425 430  
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His  
 435 440 445  
 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly  
 450 455 460  
 Gly Ala Val Pro  
 465

<210> 5

<211> 477

<212> PRT

<213> Aequorea victoria

<400> 5

Met 1	Ser	Lys	Gly	Glu 5	Glu	Leu	Phe	Thr	Gly 10	Val	Val	Pro	Ile	Leu 15	Val
Glu	Leu	Asp	Gly 20	Asp	Val	Asn	Gly	His 25	Lys	Phe	Ser	Val	Ser 30	Gly	Glu
Gly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys
Thr	Thr 50	Gly	Lys	Leu	Pro	Val 55	Pro	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Leu
Thr 65	Tyr	Gly	Val	Gln	Cys 70	Phe	Ser	Arg	Tyr	Pro 75	Asp	His	Met	Lys	Gln 80
His	Asp	Phe	Phe 85	Lys	Ser	Ala	Met	Pro	Glu 90	Gly	Tyr	Val	Gln	Glu 95	Arg
Thr	Ile	Phe	Phe 100	Lys	Asp	Asp	Gly	Asn 105	Tyr	Lys	Thr	Arg	Ala 110	Glu	Val
Lys	Phe 115	Glu	Gly	Asp	Thr	Leu	Val 120	Asn	Arg	Ile	Glu 125	Leu	Lys	Gly	Ile
Asp 130	Phe	Lys	Glu	Asp	Gly	Asn 135	Ile	Leu	Gly	His	Lys 140	Leu	Glu	Tyr	Asn
Tyr 145	Asn	Ser	His	Asn	Val 150	Tyr	Ile	Met	Ala	Asp 155	Lys	Gln	Lys	Asn	Gly 160
Ile	Lys	Ala	Asn 165	Phe	Lys	Ile	Arg	His 170	Asn	Ile	Glu	Asp	Gly	Ser 175	Val
Gln	Leu	Ala 180	Asp	His	Tyr	Gln	Gln	Asn 185	Thr	Pro	Ile	Gly	Asp 190	Gly	Pro
Val	Leu 195	Leu	Pro	Asp	Asn	His	Tyr 200	Leu	Ser	Thr	Gln	Ser 205	Ala	Leu	Ser
Lys 210	Asp	Pro	Asn	Glu	Lys	Arg 215	Asp	His	Met	Val	Leu 220	Leu	Glu	Phe	Val
Thr 225	Ala	Ala	Gly	Ile	Thr 230	His	Gly	Met	Asp	Glu 235	Leu	Tyr	Lys	Ser	Gly 240
Gly	Ser	Gly	Ser 245	Gly	Gly	Gln	Ser	Gly	Gly 250	Ser	Gly	Ser	Gly	Gly 255	Gln
Ser	Gly	Gly	Ser 260	Gly	Ser	Gly	Gly	Gln 265	Ser	Gly	Gly	Ser	Gly 270	Ser	Gly
Gly	Gln	Ser 275	Gly	Gly	Ser	Gly	Ser	Gly 280	Gly	Gln	Ser	Gly 285	Leu	Arg	Ser
Val 290	Lys	Leu	Thr	Ser	Asp	Phe 295	Asp	Asn	Pro	Arg	Trp 300	Ile	Gly	Arg	His



Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser  
 305 310 315 320  
 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu  
 325 330 335  
 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala  
 340 345 350  
 Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro  
 355 360 365  
 Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys  
 370 375 380  
 Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu  
 385 390 395 400  
 Phe Asp Ile Val Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu  
 405 410 415  
 Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp  
 420 425 430  
 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu  
 435 440 445  
 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met  
 450 455 460  
 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro  
 465 470 475

<210> 6  
 <211> 906  
 <212> PRT  
 <213> Aequorea victoria

<400> 6  
 Met Val Ser Ala Ser Arg Pro Glu Ala Leu Ala Ala Pro Val Thr Thr  
 1 5 10 15  
 Val Ala Thr Leu Val Pro His Asn Ala Thr Glu Pro Ala Ser Pro Gly  
 20 25 30  
 Glu Gly Lys Glu Asp Ala Phe Ser Lys Leu Lys Gln Lys Phe Met Asn  
 35 40 45  
 Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile Ala  
 50 55 60  
 Ile Val Ala Val Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys  
 65 70 75 80  
 Lys Cys Leu Phe Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys Gly  
 85 90 95

Gly	Lys	Asn	Ala	Ile	Asn	Met	Lys	Asp	Val	Lys	Asp	Leu	Gly	Lys	Thr	100	105	110	
Met	Lys	Asp	Gln	Ala	Leu	Lys	Asp	Asp	Asp	Ala	Glu	Thr	Gly	Leu	Thr	115	120	125	
Asp	Gly	Glu	Glu	Lys	Glu	Glu	Pro	Lys	Glu	Glu	Glu	Lys	Leu	Gly	Lys	130	135	140	
Leu	Gln	Tyr	Ser	Leu	Asp	Tyr	Asp	Phe	Gln	Asn	Asn	Gln	Leu	Leu	Val	145	150	155	160
Gly	Ile	Ile	Gln	Ala	Ala	Glu	Leu	Pro	Ala	Leu	Asp	Met	Gly	Gly	Thr	165	170	175	
Ser	Asp	Pro	Tyr	Val	Lys	Val	Phe	Leu	Leu	Pro	Asp	Lys	Lys	Lys	Lys	180	185	190	
Phe	Glu	Thr	Lys	Val	His	Arg	Lys	Thr	Leu	Asn	Pro	Val	Phe	Asn	Glu	195	200	205	
Gln	Phe	Thr	Phe	Lys	Val	Pro	Tyr	Ser	Glu	Leu	Gly	Gly	Lys	Thr	Leu	210	215	220	
Val	Met	Ala	Val	Tyr	Asp	Phe	Asp	Arg	Phe	Ser	Lys	His	Asp	Ile	Ile	225	230	235	240
Gly	Glu	Phe	Lys	Val	Pro	Met	Asn	Thr	Val	Asp	Phe	Gly	His	Val	Thr	245	250	255	
Glu	Glu	Trp	Arg	Asp	Leu	Gln	Ser	Ala	Glu	Lys	Glu	Glu	Gln	Glu	Lys	260	265	270	
Leu	Gly	Asp	Ile	Cys	Phe	Ser	Leu	Arg	Tyr	Val	Pro	Thr	Ala	Gly	Lys	275	280	285	
Leu	Thr	Val	Val	Ile	Leu	Glu	Ala	Lys	Asn	Leu	Lys	Lys	Met	Asp	Val	290	295	300	
Gly	Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	Ile	His	Leu	Met	Gln	Asn	Gly	305	310	315	320
Lys	Arg	Leu	Lys	Lys	Lys	Lys	Thr	Thr	Ile	Lys	Lys	Asn	Thr	Leu	Asn	325	330	335	
Pro	Tyr	Tyr	Asn	Glu	Ser	Phe	Ser	Phe	Glu	Val	Pro	Phe	Glu	Gln	Ile	340	345	350	
Gln	Lys	Val	Gln	Val	Val	Val	Thr	Val	Leu	Asp	Tyr	Asp	Lys	Ile	Gly	355	360	365	
Lys	Asn	Asp	Ala	Ile	Gly	Lys	Val	Phe	Val	Gly	Tyr	Asn	Ser	Thr	Gly	370	375	380	
Ala	Glu	Leu	Arg	His	Trp	Ser	Asp	Met	Leu	Ala	Asn	Pro	Arg	Arg	Pro	385	390	395	400

Ile	Ala	Gln	Trp	His	Thr	Leu	Gln	Val	Glu	Glu	Glu	Val	Asp	Ala	Met			
				405					410					415				
Leu	Ala	Val	Lys	Arg	Ser	Gly	Asn	Ser	Gly	Arg	Ala	Thr	Met	Ser	Lys			
			420					425					430					
Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp			
		435					440					445						
Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly			
	450					455					460							
Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly			
465					470					475					480			
Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly			
				485					490					495				
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe			
			500					505					510					
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe			
		515					520					525						
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu			
	530					535					540							
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys			
545					550					555					560			
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser			
			565						570					575				
His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala			
			580					585					590					
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala			
		595					600					605						
Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu			
	610					615					620							
Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro			
625					630					635					640			
Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala			
			645					650						655				
Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Gly	Gly	Ser	Gly			
			660				665						670					
Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly			
		675					680					685						
Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser			
	690					695					700							

Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu Arg Ser Val Lys Leu  
 705 710 715 720  
 Thr Ser Asp Phe Asp Asn Pro Arg Trp Ile Gly Arg His Lys His Met  
 725 730 735  
 Phe Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser Leu Asp Glu  
 740 745 750  
 Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu Gly Ala Thr  
 755 760 765  
 Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala Phe Phe Gly  
 770 775 780  
 Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile  
 785 790 795 800  
 Glu Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys  
 805 810 815  
 Asn Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile  
 820 825 830  
 Val Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala  
 835 840 845  
 Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu  
 850 855 860  
 Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu Asp Val Asp  
 865 870 875 880  
 Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala  
 885 890 895  
 Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro  
 900 905

<210> 7

<211> 3973

<212> DNA

<213> *Aequorea victoria*

<400> 7

atgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctgggtcga gctggacggc 60  
 gacgtaaacg gccacaagtt cagcgtgtcc ggcgaggggc agggcgatgc cacctacggc 120  
 aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gccaccctc 180  
 gtgaccaccc tgacctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag 240  
 cactgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgcac catctttctt 300  
 aaggacgacg gcaactacaa gaccgcgcgc gaggtgaagt tcgagggcga caccctggtg 360  
 aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 420  
 ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc 480  
 atcaaggcca acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 540  
 cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 600  
 ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 660  
 ctggagttcg tgaccgcgcg cgggatcact cactggcatgg acgagctgta caagtccgga 720

ctcagatctg	tcaaacttac	atcagacttc	gacaacccaa	gatggattgg	acgacacaag	780
catatgttca	atttccttga	tgtcaaccac	aatggaaaaa	tctctcttga	cgagatggtc	840
tacaaggcat	ctgatattgt	catcaataac	cttggagcaa	cacctgagca	agccaaacga	900
cacaaagatg	ctgtggaagc	cttcttcgga	ggagctggaa	tgaatatatg	tgtggaaact	960
gattggcctg	catatatgtg	aggatggaaa	aaattggcta	ctgatgaatt	ggagaaatac	1020
gccaaaaacg	aaccaaccct	catccgcata	tggggtgatg	ctttgtttga	tatcgttgac	1080
aaagatcaaa	atggagctat	tacactggat	gaatggaaa	catacaccaa	agctgctgg	1140
atcatccaat	catcagaaga	ttgcgaggaa	acattcagag	tgtgcatat	tgatgaaagt	1200
ggacaactcg	atgttgatga	gatgacaaga	cagcatctgg	gatttttggt	caccatggat	1260
cctgcttgcg	aaaagctcta	cgggtggagct	gtccccgaat	gagcaagggc	gaggagctgt	1320
tcaccggggg	ggtgcccctc	ctggtcgagc	tggacggcga	cgtaaacggc	cacaagttca	1380
gcgtgtccgg	cgagggcgag	ggcgatgcca	cctacggcaa	gctgaccctg	aagttcattc	1440
gcaccaccgg	caagctggcc	gtgccctggc	ccaccctcgt	gaccaccctg	acctacggcg	1500
tgcaagtctt	cagccgctac	cccgaaccaca	tgaagcagca	cgacttcttc	aagtcgcgca	1560
tgcccgaagg	ctacgtccag	gagcgcacca	tcttcttcaa	ggacgacggc	aactacaaga	1620
cccgcgccga	ggtgaagttc	gagggcgaca	ccctggtgaa	ccgcatcgag	ctgaagggca	1680
tcgacttcaa	ggaggacggc	aacatcctgg	ggcacaagct	ggagtacaac	tacaacagcc	1740
acaacgtcta	tatcatggcc	gacaagcaga	agaacggcat	caaggccaac	ttcaagatcc	1800
gccacaacat	cgaggacggc	agcgtgcagc	tcgccgacca	ctaccagcag	aacaccccca	1860
tcggcgacgg	ccccgtgctg	ctgcccgcga	accactacct	gagcaccag	tccgccctga	1920
gcaaagaccc	caacgagaag	cgcgatcaca	tggtcctgct	ggagttcgtg	accgcgcg	1980
ggatcactca	cggcatggac	gagctgtaca	agtcggcg	gagcggatcc	ggcggccagt	2040
ccggcctcag	atctgtcaaa	cttacatcag	acttcgacaa	ccaagatgg	attggacgac	2100
acaagcatat	gttcaatttc	cttgatgtca	accacaatgg	aaaaatctct	cttgacgaga	2160
tggtctacaa	ggcatctgat	attgtcatca	ataaccttgg	agcaacacct	gagcaagcca	2220
aacgacacaa	agatgctgtg	gaagccttct	tcggaggagc	tggaatgaaa	tatgggtgtg	2280
aaactgattg	gcctgcatat	attgaaggat	ggaaaaaatt	ggctactgat	gaattggaga	2340
aatacgccaa	aaacgaacca	accctcatcc	gcatatgggg	tgatgctttg	tttgatatcg	2400
ttgacaaaga	tcaaaatgga	gctattacac	tggatgaatg	gaaagcatac	accaaagctg	2460
ctggatcat	ccaatcatca	gaagattgcg	aggaaacatt	cagagtgtgc	gatattgatg	2520
aaagtggaca	actcgatgtt	gatgagatga	caagacagca	tctgggattt	tggtacacca	2580
tggtccctgc	ttgcgaaaag	ctctacggtg	gagctgtccc	cgaatgagca	agggcgagga	2640
gctgttcacc	gggggtggtg	ccatcctggt	cgagctggac	ggcgacgtaa	acggccacaa	2700
gttcagcgtg	tccggcgagg	gcgagggcga	tgccacctac	ggcaagctga	ccctgaagtt	2760
catctgcacc	accggcaagc	tgcccgtgcc	ctggcccacc	ctcgtgacca	ccctgacct	2820
cggcgtgcag	tgcttcagcc	gctaccccga	ccacatgaag	cagcacgact	tcttcaagtc	2880
cgccatgccc	gaaggctacg	tccaggagcg	caccatcttc	ttcaaggacg	acggcaacta	2940
caagaccgcg	gccgaggtga	agttcgaggg	cgacaccctg	gtgaaccgca	tcgagctgaa	3000
gggcatcgac	ttcaaggagg	acggcaacat	cctggggcac	aagctggagt	acaactacaa	3060
cagccacaac	gtctatatca	tggccgacaa	gcagaagaac	ggcatcaagg	ccaacttcaa	3120
gatccgccac	aacatcgagg	acggcagcgt	gcagctcgcc	gaccactacc	agcagaacac	3180
ccccatcggc	gacggccccg	tgctgctgcc	cgacaaccac	tacctgagca	cccagtccgc	3240
cctgagcaaa	gaccccaacg	agaagcgcg	tcacatggtc	ctgctggagt	tcgtgaccgc	3300
cgccgggatc	actcacggca	tggacgagct	gtacaagtcc	ggcgggagcg	gatccggcg	3360
ccagtccggc	gggagcggat	ccggcggcca	gtccggcctc	agatctgtca	aacttacatc	3420
agacttcgac	aacccaagat	ggattggacg	acacaagcat	atgttcaatt	tccttgatgt	3480
caaccacaat	ggaaaaatct	ctcttgacga	gatggtctac	aaggcatctg	atattgtcat	3540
caataacctt	ggagcaacac	ctgagcaagc	caaacgacac	aaagatgctg	tggaagcctt	3600
cttcggagga	gctggaatga	aatatggtgt	cgaaaactgat	tggcctgcat	atattgaagg	3660
atggaaaaaa	ttggctactg	atgaattgga	gaaatacgcc	aaaaacgaac	caaccctcat	3720
ccgcatatgg	ggtgatgctt	tgtttgatat	cgttgacaaa	gatcaaaatg	gagctattac	3780
actggatgaa	tggaaagcat	acaccaaaag	tgctggtatc	atccaatcat	cagaagattg	3840
cgaggaaaca	ttcagagtgt	gcgatattga	tgaagtgga	caactcgatg	ttgatgagat	3900
gacaagacag	catctgggat	tttggtacac	catggatcct	gcttgcgaaa	agctctacgg	3960
tggagctgtc	ccc					3973

<210> 8  
 <211> 2673  
 <212> DNA  
 <213> *Aequorea victoria*

<400> 8  
 atgagcaagg gcgaggagct gttcaccggg gtggtgccc tcttggtcga gctggacggc 60  
 gacgtaaacy gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 120  
 aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 180  
 gtgaccaccc tgacctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag 240  
 cagcacttct tcaagtccgc catgcccga ggctacgtcc aggagcgcac catcttcttc 300  
 aaggacgacg gcaactacaa gacccgcgcc gaggtgaagt tcgagggcga caccctggtg 360  
 aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 420  
 ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc 480  
 atcaaggcca acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 540  
 cactaccagc agaacacccc catcgccgac ggccccgtgc tgctgcccga caaccactac 600  
 ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 660  
 ctggagtctg tgaccgccgc cgggatcact cacggcatgg acgagctgta caagtccggc 720  
 gggagcggat ccggcggcca gtccggcctc agatctgtca aacttacatc agacttcgac 780  
 aacccaagat ggattggacg acacaagcat atgttcaatt tccttgatgt caaccacaat 840  
 ggaaaaatct ctcttgacga gatggtctac aaggcatctg atattgtcat caataacctt 900  
 ggagcaacac ctgagcaagc caaacgacac aaagatgctg tggaagcctt cttcggagga 960  
 gctggaatga aatatggtgt ggaaactgat tggcctgcat atattgaagg atggaaaaaa 1020  
 ttggctactg atgaattgga gaaatacgcc aaaaacgaac caaccctcat ccgcatatgg 1080  
 ggtgatgctt tgtttgatat cgttgacaaa gatcaaaatg gagctattac actggatgaa 1140  
 tggaaagcat acaccaaagc tgctggtatc atccaatcat cagaagattg cgaggaaaca 1200  
 ttcagagtgt gcgatattga tgaaagtgga caactcgatg ttgatgagat gacaagacag 1260  
 catctgggat tttggtacac catggatcct gcttgcgaaa agctctacgg tggagctgtc 1320  
 cccatgagca agggcgagga gctgttcacc ggggtggtgc ccactctggt cgagctggac 1380  
 ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 1440  
 ggcaagctga cctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 1500  
 ctctgtacca cctgaccta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 1560  
 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 1620  
 ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg 1680  
 gtgaaccgca tcgagctgaa gggcacgac ttcaaggagg acggcaacat cctggggcac 1740  
 aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 1800  
 ggcacaaagg ccaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 1860  
 gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 1920  
 tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 1980  
 tcgctggagt tcgtgacgcg cgccgggatc actcacggca tggacgagct gtacaagtcc 2040  
 ggccggagcg cactccggcg ccagtccggc gggagcggat ccggcggcca gtccggcctc 2100  
 agatctgtca aacttacatc agacttcgac aacccaagat ggattggacg acacaagcat 2160  
 atgttcaatt tccttgatgt caaccacaat ggaaaaatct ctcttgacga gatggtctac 2220  
 aaggcatctg atattgtcat caataacctt ggagcaacac ctgagcaagc caaacgacac 2280  
 aaagatgctg tggaagcctt cttcggagga gctggaatga aatatggtgt ggaaactgat 2340  
 tggcctgcat atattgaagg atggaaaaaa ttggctactg atgaattgga gaaatacgcc 2400  
 aaaaacgaac caaccctcat ccgcatatgg ggtgatgctt tgtttgatat cgttgacaaa 2460  
 gatcaaaatg gagctattac actggatgaa tggaaagcat acaccaaagc tgctggtatc 2520  
 atccaatcat cagaagattg cgaggaaaca ttcagagtgt gcgatattga tgaaagtgga 2580  
 caactcgatg ttgatgagat gacaagacag catctgggat tttggtacac catggatcct 2640  
 gcttgcgaaa agctctacgg tggagctgtc ccc 2673

<210> 9  
 <211> 1350  
 <212> DNA  
 <213> *Aequorea victoria*

&lt;400&gt; 9

```

atgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctgggtcga gctggacggc 60
gacgtaaacc gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 120
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 180
gtgaccaccc tgacctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag 240
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgcac catcttcttc 300
aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg 360
aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 420
ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc 480
atcaaggcca acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 540
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 600
ctgagcacc cagtcgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 660
ctggagtctc tgaccgcgc cgggatcact cacggcatgg acgagctgta caagtccggc 720
gggagcggat ccggcggcca gtccggcggg agcggatccg gcggccagtc cggcctcaga 780
tctgtcaaac ttacatcaga cttcgacaac ccaagatgga ttggacgaca caagcatatg 840
ttcaatttcc ttgatgtcaa ccacaatgga aaaatctctc ttgacgagat ggtctacaag 900
gcatctgata ttgtcatcaa taaccttgga gcaacacctg agcaagccaa acgacacaaa 960
gatgctgtgg aagccttctt cggaggagct ggaatgaaat atggtgtgga aactgattgg 1020
cctgcatata ttgaaggatg gaaaaaattg gctactgatg aattggagaa atacgccaaa 1080
aacgaaccaa ccctcatccg catatggggg gatgctttgt ttgatatcgt tgacaaagat 1140
caaatggag ctattacact ggatgaatgc aaagcataca ccaaagctgc tggatcatc 1200
caatcatcag aagattgcga ggaaacattc agagtgtgcy atattgatga aagtggacaa 1260
ctcgatgttg atgagatgac aagacagcat ctgggatttt ggtacaccat ggatcctgct 1320
tgcgaaaagc tctacggtgg agctgtcccc                                     1350

```

&lt;210&gt; 10

&lt;211&gt; 1404

&lt;212&gt; DNA

<213> *Aequorea victoria*

&lt;400&gt; 10

```

atgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctgggtcga gctggacggc 60
gacgtaaacc gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 120
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 180
gtgaccaccc tgacctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag 240
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgcac catcttcttc 300
aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg 360
aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 420
ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc 480
atcaaggcca acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 540
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 600
ctgagcacc cagtcgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 660
ctggagtctc tgaccgcgc cgggatcact cacggcatgg acgagctgta caagtccggc 720
gggagcggat ccggcggcca gtccggcggg agcggatccg gcggccagtc cggcgggagc 780
ggatccggcg gccagtccgg cgggagcggg tccggcggcc agtccggcct cagatctgtc 840
aaacttacat cagacttcga caaccacaaga tggattggac gacacaagca tatgttcaat 900
ttccttgatg tcaaccacaa tggaaaaatc tctcttgacg agatggtcta caaggcatct 960
gatattgtca tcaataacct tggagcaaca cctgagcaag ccaaacgaca caaagatgct 1020
gtggaagcct tcttcggagg agctggaatg aaatatggtg tggaaactga ttggcctgca 1080
tatattgaag gatggaaaaa attggctact gatgaattgg agaaatacgc caaaaacgaa 1140
ccaaccctca tccgcatatg gggatgatgt ttgtttgata tcgttgacaa agatcaaaat 1200
ggagctatta cactggatga atggaaagca tacaccaaaag ctgctggtat catccaatca 1260
tcagaagatt gcgaggaaac attcagagtg tgcgatattg atgaaagtgg acaactcgat 1320
gttgatgaga tgacaagaca gcatctggga ttttggtaca ccatggatcc tgcttgcgaa 1380
aagctctacg gtggagctgt cccc                                     1404

```

<210> 11  
 <211> 1431  
 <212> DNA  
 <213> *Aequorea victoria*

<400> 11  
 atgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctgggtcga gctggacggc 60  
 gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 120  
 aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 180  
 gtgaccaccc tgacctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag 240  
 cagcacttct tcaagtccgc catgcccga ggctacgtcc aggagcgcac catcttcttc 300  
 aaggacgacg gcaactacaa gacccgcgcc gaggtgaagt tcgagggcga caccctgggtg 360  
 aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 420  
 ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc 480  
 atcaaggcca acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 540  
 cactaccagc agaacacccc catcgccgac ggccccgtgc tgctgcccga caaccactac 600  
 ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catgggtcctg 660  
 ctggagtctg tgaccgccgc cgggatcact cacggcatgg acgagctgta caagtccggc 720  
 gggagcggat ccggcggcca gtccggcggg agcggatccg gcggccagtc cggcggggagc 780  
 ggatccggcg gccagtccgg cgggagcgga tccggcgggc agtccggcgg gagcggatcc 840  
 ggcggccagt ccggcctcag atctgtcaaa cttacatcag acttcgacaa cccaagatgg 900  
 attggacgac acaagcatat gttcaatttc cttgatgtca accacaatgg aaaaatctct 960  
 cttgacgaga tggctacaa ggcatctgat attgtcatca ataaccttgg agcaacacct 1020  
 gagcaagcca aacgacacaa agatgctgtg gaagccttct tcggaggagc tggaatgaaa 1080  
 tatggtgtgg aaactgattg gcctgcatat attgaaggat ggaaaaaatt ggctactgat 1140  
 gaattggaga aatacgccaa aaacgaacca accctcatcc gcatatgggg tgatgctttg 1200  
 tttgatatcg ttgacaaaga tcaaaatgga gctattacac tggatgaatg gaaagcatat 1260  
 accaaagctg ctggtatcat ccaatcatca gaagattgcg aggaaacatt cagagtgtgc 1320  
 gatattgatg aaagtggaca actcgatgtt gatgagatga caagacagca tctgggattt 1380  
 tggtagacca tggatcctgc ttgcgaaaag ctctacgggtg gagctgtccc c 1431

<210> 12  
 <211> 2718  
 <212> DNA  
 <213> *Aequorea victoria*

<400> 12  
 atgggtgagt ccagtcgtcc tgaggccctg gctgcccctg tcaccactgt tgcgaccctt 60  
 gtccacacata acgccactga gccagccagt cctggggaag ggaaggaaga tgccttttcc 120  
 aagctgaagc agaagtttat gaatgaactg cataaaatcc cattgccacc gtgggcctta 180  
 attgccatag ccatagttgc ggtccttcta gtcgtgacct gctgcttctg tgtctgtaag 240  
 aaatgtttgt tcaaaaagaa aaacaagaag aagggaaggg aaaaggaggg gaagaacgcc 300  
 attaacatga aagacgtgaa agacttaggg aagaccatga aggatcaggc ccttaaggat 360  
 gacgatgctg aaactggact gactgatgga gaagaaaagg aggagcccaa ggaagaggag 420  
 aaactgggaa agcttcaata ttactggac tatgacttcc agaataacca gctgctggtg 480  
 ggaatcatcc aggtctgtga actgcccgcc ctggacatgg gaggcacatc tgatccatac 540  
 gtcaaagtct tcctgctgcc cgacaaaaag aagaagtttg agacaaaagt ccaccggaaa 600  
 accctcaatc cagtcttcaa tgaacagttt actttcaagg tgccatactc ggaattaggt 660  
 ggcaagacac tgggtgatggc tgtgtatgat tttgaccgct tctccaagca cgacatcatt 720  
 ggagagttca aagttcctat gaacaccgtg gattttggcc acgtcaccca ggagtggcgc 780  
 gatctccaga gtgctgagaa agaagagcaa gagaaactgg gtgacatctg cttctccctc 840  
 cgctacgtcc ctactgccgg caagctgact gttgtcattc tggaagccaa gaacctgaag 900  
 aagatggatg tgggtggctt atctgatccc tatgtaaaga ttcacctgat gcagaacggc 960  
 aagagactga agaagaaaaa gacaacgatt aagaagaaca cacttaaccc ctactacaat 1020  
 gagtccctca gctttgaagt tccgttcgag caaatccaga aagtgaaggt ggtggtaact 1080  
 gttttggact atgacaagat tggcaagaac gacgccatcg gcaaagtctt tgtgggctac 1140  
 aacagcaccg gcgcagagct gcgacactgg tcagacatgc tggccaaccc ccggcgaccc 1200



```

atcgcccagt ggcacactct gcaggtagag gaggagggtt atgccatgct ggctgtcaag 1260
agatccggga attccgggcg ggccaccatg agcaaggcg aggagctgtt caccggggtg 1320
gtgcccattc tggtcgagct ggacggcgac gtaaacggcc acaagttcag cgtgtccggc 1380
gagggcgagg gcgatgccac ctacggcaag ctgaccctga agttcatctg caccaccggc 1440
aagctgcccc tgccctggcc caccctcggt accaccctga cctacggcgt gcagtgttcc 1500
agccgctacc ccgaccacat gaagcagcac gactttcttca agtccgcat gcccgaaggc 1560
tacgtccagg agcgcacat cttcttcaag gacgacggca actacaagac ccgcgccgag 1620
gtgaagtctg agggcgacac cctggtgaac cgcacgagc tgaaggcat cgacttcaag 1680
gaggacggca acatcctggg gcacaagctg gagtacaact acaacagcca caacgtctat 1740
atcatggccg acaagcagaa gaacggcatc aaggccaact tcaagatccg ccacaacatc 1800
gaggacggca gcgtgcagct cgccgaccac taccagcaga acaccccat cggcgacggc 1860
cccgtgtgct tgcccgacaa ccactacctg agcaccagt ccgccctgag caaagacccc 1920
aacgagaagc gcgatcacat ggtcctgctg aggttcgtga ccgcgcggg gatcactcac 1980
ggcatggacg agctgtacaa gtccggcggg agcggatccg gcggccagtc cggcgggagc 2040
ggatccggcg gccagtccgg cgggagcgga tccggcgggc agtccggcgg gagcggtacc 2100
ggcgggcagt ccggcgggag cggatccggc ggccagtccg gcctcagatc tgtcaaactt 2160
acatcagact tcgacaaccc aagatggatt ggacgacaca agcatatgtt caatttcctt 2220
gatgtcaacc acaatggaaa aatctctctt gacgagatgg tctacaaggc atctgatatt 2280
gtcatcaata accttgagc aacacctgag caagccaaac gacacaaaga tgctgtggaa 2340
gccttcttcg gaggagctgg aatgaaatat ggtgtggaaa ctgattggcc tgcataatatt 2400
gaaggatgga aaaaattggc tactgatgaa ttggagaaat acgcaaaaaa cgaaccaacc 2460
ctcatccgca tatgggtgta tgctttgttt gatatcgttg acaaagatca aaatggagct 2520
attacactgg atgaatggaa agcatacacc aaagctgctg gtatcatcca atcatcagaa 2580
gattgcgagg aaacattcag agtggtcgat attgatgaaa gtggacaact cgatgttgat 2640
gagatgacaa gacagcatct gggatttttg tacaccatgg atcctgcttg cgaaaagctc 2700
tacggtggag ctgtcccc 2718

```

<210> 13

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
of GFP-aequorin linker

<400> 13

tccggcctca gatct

15

<210> 14

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
of GFP-aequorin linker

<400> 14

tccggcgggga gcggatccgg cggccagtcc ggccctcagat ct

42

<210> 15

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
of GFP-aequorin linker

<400> 15

tccggcggga gcggatccgg cggccagtcc ggcgggagcg gatccggcgg ccagtccggc 60  
ctcagatct 69

<210> 16

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
of GFP-aequorin linker

<400> 16

tccggcggga gcggatccgg cggccagtcc ggcgggagcg gatccggcgg ccagtccggc 60  
gggagcggat ccggcggcca gtccggcggg agcggatccg gcggccagtc cggcctcaga 120  
tct 123

<210> 17

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
of GFP-aequorin linker

<400> 17

tccggcggga gcggatccgg cggccagtcc ggcgggagcg gatccggcgg ccagtccggc 60  
gggagcggat ccggcggcca gtccggcggg agcggatccg gcggccagtc cggcgggagc 120  
ggatccggcg gccagtccgg cctcagatct 150

<210> 18

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide  
sequence of linker

<400> 18

Ser Gly Leu Arg Ser

1

5

<210> 19

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide  
sequence of linker

<400> 19

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu Arg Ser  
1 5 10

<210> 20

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide  
sequence of linker

<400> 20

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly  
1 5 10 15

Gly Gln Ser Gly Leu Arg Ser  
20

<210> 21

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide  
sequence of linker

<400> 21

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly  
1 5 10 15

Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly  
20 25 30

Ser Gly Gly Gln Ser Gly Leu Arg Ser  
35 40

<210> 22

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide  
sequence of linker

&lt;400&gt; 22

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly  
 1 5 10 15

Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly  
 20 25 30

Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu  
 35 40 45

Arg Ser  
 50

&lt;210&gt; 23

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

&lt;400&gt; 23

ccggcgaggag cggatccggc ggccagt

27

&lt;210&gt; 24

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

&lt;400&gt; 24

ccggactggc cgccggatcc gctcccg

27

&lt;210&gt; 25

&lt;211&gt; 45

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Linker

&lt;220&gt;

<223> This sequence may encompass either 9, 18, 27, 36,  
 or 45 amino acids, with 9 or 45 amino acids being  
 more preferable

&lt;400&gt; 25

Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly  
 1 5 10 15

Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser  
                           20                          25                          30

Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser  
           35                          40                          45

<210> 26  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Linker

<400> 26  
 Ser Gly Leu Arg Ser  
       1                          5

<210> 27  
 <211> 27  
 <212> DNA  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: pEGFP-C1 plasmid

<400> 27  
 gtcgacggta ccgcgggccc gggatcc

27

<210> 28  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Illustrative  
           nucleic acid

<400> 28  
 gtcgacgggg atcc

14

<210> 29  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           construct

<220>  
 <221> CDS  
 <222> (19)..(33)

&lt;400&gt; 29

gcgctaccgc gggccacc atg agc aag ggc gag  
 Met Ser Lys Gly Glu  
 1 5

33

&lt;210&gt; 30

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 construct

&lt;400&gt; 30

Met Ser Lys Gly Glu  
 1 5

&lt;210&gt; 31

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Aequorea victoria

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (19)..(36)

&lt;400&gt; 31

gcgctaccgg tcgccacc atg gtg agc aag ggc gag  
 Met Val Ser Lys Gly Glu  
 1 5

36

&lt;210&gt; 32

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Aequorea victoria

&lt;400&gt; 32

Met Val Ser Lys Gly Glu  
 1 5

&lt;210&gt; 33

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 construct

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3)..(20)

<400> 33  
 gc atc aag gcc aac ttc aag  
 Ile Lys Ala Asn Phe Lys  
 1 5

20

<210> 34  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 construct

<400> 34  
 Ile Lys Ala Asn Phe Lys  
 1 5

<210> 35  
 <211> 20  
 <212> DNA  
 <213> Aequorea victoria

<220>  
 <221> CDS  
 <222> (3)..(20)

<400> 35  
 gc atc aag gtg aac ttc aag  
 Ile Lys Val Asn Phe Lys  
 1 5

20

<210> 36  
 <211> 6  
 <212> PRT  
 <213> Aequorea victoria

<400> 36  
 Ile Lys Val Asn Phe Lys  
 1 5

<210> 37  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 construct

<220>  
 <221> CDS  
 <222> (3)..(17)

<400> 37  
 gg atc act cac ggc atg ga  
 Ile Thr His Gly Met  
 1 5

19

<210> 38  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 construct

<400> 38  
 Ile Thr His Gly Met  
 1 5

<210> 39  
 <211> 19  
 <212> DNA  
 <213> Aequorea victoria

<220>  
 <221> CDS  
 <222> (3)..(17)

<400> 39  
 gg atc act ctc ggc atg ga  
 Ile Thr Leu Gly Met  
 1 5

19

<210> 40  
 <211> 5  
 <212> PRT  
 <213> Aequorea victoria

<400> 40  
 Ile Thr Leu Gly Met  
 1 5

<210> 41  
 <211> 596  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Altered  
 Aequoria victoria sequence

<400> 41  
 agcttcagat ctgtcaaact tacatcagac ttcgacaacc caagatggat tggacgacac 60  
 aagcatatgt tcaatttcct tgatgtcaac cacaatggaa aaatctctct tgacgagatg 120  
 gtctacaagg catctgatat tgatcatcaat aaccttggag caacacctga gcaagccaaa 180



```

cgacacaaag atgctgtgga agccttcttc ggaggagctg gaatgaaata tgggtgtggaa 240
actgattggc ctgcatatat tgaaggatgg aaaaaattgg ctactgatga attggagaaa 300
tacgccaaaa acgaaccaac cctcatccgc atctgggggtg atgctttgtt tgatatcgtt 360
gacaaagatc aaaatggagc tattacactg gatgaatgga aagcatacac caaagctgct 420
ggtatcatcc aatcatcaga agattgcgag gaaacattca gagtgtgcga tattgatgaa 480
agtggacaac tcgatgttga tgagatgaca agacagcatc tgggattttg gtacaccatg 540
gatcctgctt gcgaaaagct ctacggtgga gctgtcccct aatctcgagg atcttt 596

```

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
construct

<220>

<221> CDS

<222> (1)..(21)

<400> 42

aag tcc gga ctc aga tct gtc

21

Lys Ser Gly Leu Arg Ser Val

1

5

<210> 43

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
construct

<400> 43

Lys Ser Gly Leu Arg Ser Val

1

5

<210> 44

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
construct

<400> 44

gacagatctg agtccggact t

21

<210> 45

<211> 21

<212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 construct

<400> 45  
 aagtgcggac tcagatctgt c

21

<210> 46  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 construct

<400> 46  
 ccggcgggag cggatccggc ggccagt

27

<210> 47  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 construct

<400> 47  
 Gly Gly Ser Gly Ser Gly Gly Gln Ser  
 1 5

<210> 48  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 construct

<400> 48  
 ccggactggc cgccggatcc gctcccg

27